REMARKS

Reconsideration is respectfully requested. Claims 1-18, 26, and 33-50 were pending in this application. Claim 26 has been allowed. Claims 1, 15, 33, and 48 have been amended to more particularly point out the subject matter of the Applicant's invention. Specifically, claim 1 has been amended to recite that the pool of test transcription factors are "cloned". Independent claim 33 has been amended to provide proper antecedent basis and place it in conformity with claim 1. Dependent claims have accordingly also been amended. After entry of this amendment, claims 1-18 and 33-50 will be under consideration.

Sequence Listing

In response to the Examiner's request, Applicants submit a new Sequence Listing.

Applicant has amended the specification to identify the Seq. ID. NOs and replace the original sequence listing with a sequence listing that complies with the sequence rules, 37 C.F.R. §§ 1.821 - 1.825.

The undersigned hereby states that the content of the attached papers and the computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

A copy of the *Notice to Comply* is attached hereto as required by United States Patent Office rules governing gene sequences.

Claim Objections

Claims 33-50 Under 35 U.S.C. §112, Paragraph 1

The Examiner states that the specification does not reasonably provide enablement for the method of claims 33-50 so that one of skill in the art would be able to determine whether two or more members of a pool of test transcription factor polynucleotides (consisting of more than four members) are required for expression from a pathway gene promoter.

The Applicant disagrees. In order to make a rejection, the Examiner has the initial burden to establish a reasonable basis to question the enablement provided for the claimed invention. MPEP 2164.04 citing *In re Wright*, 999 F.2d 1557, 1562, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993). The Examiner states that the prior art has been analyzed and that it indicates there is no well-known protocol for identifying which transcription factors from a large pool interact to activate a promoter. However, this prior art has not been disclosed to the Applicant. Therefore, the Examiner has not established a *prima facie* case of lack of enablement.

Furthermore, the Applicant submits that the claimed method is sufficiently described at page 15, lines 14-20, to permit one skilled in the art to use it. The claimed method can be used in a deconvolution process that involves repeating experiments with positive results (expression of a reporter gene), each time removing transcription factors from the pool. The experiments are repeated until the smallest set of transcription factors that produces gene activation is identified. Testing a large pool of transcription factors may become complicated and time consuming, but "the fact that experimentation may be complex does not necessarily make it undue." *In re Wands*, 858 F.2d at 737, 8 USPQ2d at 1404. Therefore, the specification does enable one of skill to make and/or use the invention commensurate in scope with these claims.

Accordingly, the Applicant respectfully requests withdrawal of the rejection.

Claims 15 and 48 Under 35 U.S.C. §112, Second Paragraph

The Examiner states that the term "high value" in claims 15 and 48 is a relative term that renders the claims indefinite. The Applicant respectfully points out that "high value secondary metabolites" is defined at page 5, lines 8-9, as those secondary metabolites that have valuable commercial applications. The terpenoids, a particularly valuable secondary metabolite class, are described on page 1, lines 18-24. Valuable commercial applications such as the manufacturing of pharmaceuticals and food additives are also described on page 1, lines 11-17. In addition, genes involved in secondary metabolite production are identified on page 7, at lines 3-16. Accordingly, it is very clear which metabolites are encompassed by the term "high value".

Nevertheless, to advance prosecution, claims 15 and 48 have been amended to remove the recitation of "high value". Therefore, after entry of the present amendment, withdrawal of the rejection is respectfully requested.

Claims 1-18 and 33-50 Under 35 U.S.C. §112, Second Paragraph

The Examiner states that a term is missing after the word "said" in line 5 of claim 1 and that there is no antecedent basis for the term "biosynthetic pathway gene promoter" in line 5 of claim 33. Claim 1 has been amended to recite that expression "of said reporter gene" is detected and claim 33 has been amended to recite "a biosynthetic pathway gene promoter" for clarity. Accordingly, after entry of the amendment, the rejection is rendered moot.

Claims 1, 10, 11, and 13 Under 35 U.S.C. §102(b)

The Examiner states that the method of claims 1, 10, 11, and 13 are anticipated by Kim et al. Kim describes an assay for detecting binding to the promoter of the carrot Dc3 gene. Screening for reporter gene expression is accomplished by introduction of uncharacterized cDNA (derived from sunflower seed RNA) into yeast cells.

The Applicant has amended claim 1 to recite that the pool contains "cloned" test transcription factors to distinguish the pool of uncharacterized cDNA described in Kim et al. Support for this amendment may be found in the specification at page 10, lines 35-36.

Therefore, after entry of the present amendment, withdrawal of the rejection is respectfully requested.

Claims 5-9 and 12 Under 35 U.S.C. §103(a)

The Examiner states that claims 5-9 and 12 are unpatentable over Kim et al. in view of WO 00/46383 ('383 patent). The Examiner admits that Kim et al. do not teach a method wherein the gene is a biosynthetic pathway gene nor a method that is carried out in plant cells. However, the Examiner states that the '383 patent describes a method of modulating metabolite synthesis in plants by transfection of cells (including plant cells) with transcription factor polynucleotides, and that one of ordinary skill would thus be motivated to use the methods described by Kim et al. to identify transcription factors involved in the biosynthesis of metabolite production in plants in order to develop methods for the increase in metabolite production.

First of all, after entry of the amendment to claim 1, as discussed *supra*, Kim et al. is no longer an anticipating reference. Thus, combining it with the '383 patent will not produce the claimed invention.

Moreover, there is no suggestion in the '383 patent to look to the methods of Kim et al. to identify transcription factors. The '383 patent describes a method for modulating biosynthetic pathway gene expression by upregulating or downregulating transcription factor expression in plant cells. Preselected transcription factor nucleotide sequences are altered or linked to a stronger or weaker promoter to modify transcription factor expression. Thus, in '383, there is no motivation to identify transcription factors using the methods of Kim et al. or any method at all because the transcription factor nucleotide sequences are already known. In contrast, the claimed method discloses a process for

determining which cloned transcription factor nucleotide sequences encode biosynthetic pathway transcription factors. Therefore, the description provided in '383 is insufficient to create a rejection under 35 U.S.C. §103(a).

Accordingly, the Applicant respectfully requests that the rejection be withdrawn.

SUMMARY

The Applicant has responded to each matter of substance raised in this Office Action. Based on the arguments expressed here, the Applicant believes the case to be patentable and requests that it be allowed.

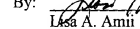
Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned **"VERSION WITH MARKING TO SHOW CHANGES MADE."**

In the event that there are any questions concerning this amendment or the application in general, the Examiner is respectfully urged to telephone the undersigned representative so that prosecution may be expedited.

In the unlikely event that the Patent Office determines that an extension and/or other relief is required as a result of this statement, Applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due to our **Deposit account no. 03-1952** referenced Docket No. **514442001200**. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: August 9, 2002

By: 

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 23, page 17 of the specification as originally filed (line 1, page 18 of the instant specification) has been amended as follows:

O30418: CGCTCTAGACCGGAACCGTCGAGCATGGTCCGTCCTGTAG (SEQ ID NO: 15), and

O30419: CGCGGATCCGCCAGGAGAGTTGTTGATTCATTGTTTGC (SEQ ID NO: 16). IntGUS makes it possible to measure GUS activity in transformed plant samples without interference from GUS activity produced by *Agrobacterium*, where the gene is inactive. The PCR product was restricted using enzymes BamHI and XbaI, and cloned into the corresponding sites of pMen065, to produce plasmid p512.

Paragraph beginning at line 32, page 17 of the specification as originally filed (line 10, page 18 of the instant specification) has been amended as follows:

O30413: ACCCAAGCTTGGGTGATATGACTTAAATATATGTACAAGTAGC (SEQ ID NO: 17) and

O30414: CGCGGATCCATTAATCTTTCCTTCCGCTCTCTTTCTATG (SEQ ID NO: 18). The resulting PCR product was cut with BamHI and HindIII and cloned into the corresponding sites of pBluescript KS, to produce plasmid p528. P528, in turn, was cut with HindIII and NotI. p512 was restricted with the same enzymes, and the vector fragment was purified away from the 35S promoter fragment. The HindIII/NotI insert fragment from p528 was ligated to this vector fragment, producing plasmid p514.

In the Claims

1. (Twice Amended) A method of determining whether a member of a pool of cloned test transcription factor polynucleotides encodes a pathway transcription factor, the method comprising introducing into a cell a nucleic acid comprising a promoter of a pathway gene operably linked to a reporter gene; [and] introducing a member of the pool

of cloned [nucleic acid members comprising] test transcription factor polynucleotides; and detecting expression [from said] of said reporter gene in the cell, thereby determining whether a member of the cloned test transcription factor polynucleotide pool encodes a pathway transcription factor.

2. (Amended) The method of claim 1, wherein a member of the cloned test transcription factor [nucleic acid] polynucleotide pool is selected on the basis of structural similarity to a known transcription factor for a pathway gene.

3. (Amended) The method of claim 1, wherein a member of the cloned test transcription factor [nucleic acid] polynucleotide pool is selected without regard to structural similarity to a known transcription factor for a pathway gene.

10. (Amended) The method of claim 1, wherein said cloned test transcription factor polynucleotide is from a plant.

11. (Amended) The method of claim 1, wherein said cloned test transcription factor polynucleotide is expressed transiently in the cell.

15. (Amended) The method of claim 1, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces [high-value] secondary metabolites.

18. (Amended) The method of claim 1, further comprising deconvoluting the pool of [nucleic acid members] cloned test transcription factor polynucleotides to identify the minimum number of cloned test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter.

33. (Twice Amended) A method of determining whether two or more members of a pool of cloned test transcription factor polynucleotides are required for expression from a pathway gene promoter, the method comprising introducing into a cell a nucleic acid comprising a [promoter of a] biosynthetic pathway gene promoter operably linked to a

reporter gene; [and] introducing a pool of [nucleic acid members comprising] cloned test transcription factor polynucleotides; and detecting expression from said biosynthetic pathway gene promoter in the cell, thereby determining whether two or more members of the cloned test transcription factor polynucleotide pool are required for expression from said promoter.

34. (Amended) The method of claim 33, further comprising deconvoluting the pool of [nucleic acid members] cloned test transcription factor polynucleotides to identify the minimum number of cloned test transcription factor polynucleotides necessary to detect expression from said pathway gene promoter.

35. (Amended) The method of claim 33, wherein a member of the cloned test transcription factor [nucleic acid] polynucleotide pool is selected on the basis of structural similarity to a known transcription factor for a pathway gene.

36. (Amended) The method of claim 33, wherein a member of the cloned test transcription factor [nucleic acid] polynucleotide pool is selected without regard to structural similarity to a known transcription factor for a pathway gene.

43. (Amended) The method of claim 33, wherein said cloned test transcription factor polynucleotide is from a plant.

44. (Amended) The method of claim 33, wherein said cloned test transcription factor polynucleotide is expressed transiently in the cell.

48. (Amended) The method of claim 33, wherein said promoter is the promoter of a biosynthetic pathway gene of a plant that produces [high-value] secondary metabolites.